#9

SEQUENCE LISTING

<110> Lanes, Olav
      Willasen, Nils Peder
      Guddal, Per Henrik
      Gjellesvik, Dag Rune

<120> Cod uracil-DNA glycosylase, gene coding therefore,
      recombinant DNA containing said gene or operative parts
      thereof, a method for preparing said protein and the
      use of said protein or said operative pa

<130> U013209-3

<140> 09/758,017
<141> 2001-01-10

<150> 2000 5428
<151> 2000-10-27

<150> 2000 0163
<151> 2000-01-12

<160> 19

<170> PatentIn Ver. 2.0

<210> 1
<211> 1283
<212> DNA
<213> Gadus morhua

<220>
<221> CDS
<222> (18)..(920)

<400> 1
gacatccgct tgcaaat atg ttg ttc aag tta ggg tta tgc caa aga tgc   50
                    Met Leu Phe Lys Leu Gly Leu Cys Gln Arg Cys
                     1   5   10

ata tca tca aat cgg gtg tta cca ggt tta cta att ccc caa act tta   98
Ile Ser Ser Asn Arg Val Leu Pro Gly Leu Leu Ile Pro Gln Thr Leu
             15   20   25

tgt ttt tct aaa tta atg aag ata acg ccg aag aaa ctg agg tcc tca   146
Cys Phe Ser Lys Leu Met Lys Ile Thr Pro Lys Lys Leu Arg Ser Ser
         30   35   40

```
aat gtg gaa caa aag acg tca tcg cca cag ctt tca gtg gag cag ctg      194
Asn Val Glu Gln Lys Thr Ser Ser Pro Gln Leu Ser Val Glu Gln Leu
    45                  50                  55

gaa aga atg gcc aaa aat aag aaa gca gcg ctt gac aag att aga gca      242
Glu Arg Met Ala Lys Asn Lys Lys Ala Ala Leu Asp Lys Ile Arg Ala
    60                  65                  70                  75

aaa gca acg cct gca ggt ttc gga gag act tgg aga aga gag ctg gct      290
Lys Ala Thr Pro Ala Gly Phe Gly Glu Thr Trp Arg Arg Glu Leu Ala
                    80                  85                  90

gca gag ttt gaa aag cca tac ttc aaa caa ttg atg tcc ttt gta gct      338
Ala Glu Phe Glu Lys Pro Tyr Phe Lys Gln Leu Met Ser Phe Val Ala
                95                  100                 105

gat gag agg agc cgt cac acc gtc tac cca ccg gct gat caa gtg tac      386
Asp Glu Arg Ser Arg His Thr Val Tyr Pro Pro Ala Asp Gln Val Tyr
        110                 115                 120

agt tcg aca gag atg tgt gac att caa gat gtg aaa gta gtg att cta      434
Ser Ser Thr Glu Met Cys Asp Ile Gln Asp Val Lys Val Val Ile Leu
        125                 130                 135

ggc cag gac cct tac cac ggt ccc aac caa gca cat gga ctc tgt ttc      482
Gly Gln Asp Pro Tyr His Gly Pro Asn Gln Ala His Gly Leu Cys Phe
140                 145                 150                 155

agt gtg caa aag cca gtt ccc cct ccc ccc agt ctc gtg aac ata tac      530
Ser Val Gln Lys Pro Val Pro Pro Pro Pro Ser Leu Val Asn Ile Tyr
                160                 165                 170

aaa gaa ttg tgt acc gac att gat ggc ttc aag cat cct gga cat gga      578
Lys Glu Leu Cys Thr Asp Ile Asp Gly Phe Lys His Pro Gly His Gly
                175                 180                 185

gat cta agc gga tgg gca aaa caa ggg gtg ctg ctg ctt aac gcg gtg      626
Asp Leu Ser Gly Trp Ala Lys Gln Gly Val Leu Leu Leu Asn Ala Val
                190                 195                 200

ctg acc gtg cgg gcc cat cag gcc aac tcc cac aag gac aga ggc tgg      674
Leu Thr Val Arg Ala His Gln Ala Asn Ser His Lys Asp Arg Gly Trp
        205                 210                 215

gag acc ttc acc gac gct gtg atc aag tgg ctg agc gtc aac cgg gaa      722
Glu Thr Phe Thr Asp Ala Val Ile Lys Trp Leu Ser Val Asn Arg Glu
220                 225                 230                 235
```

2

```
gga gtc gtt ttc ctg ttg tgg ggc tca tac gcc cat aag aag gga gcg    770
Gly Val Val Phe Leu Leu Trp Gly Ser Tyr Ala His Lys Lys Gly Ala
            240                 245                 250

acc atc gac agg aaa cgt cac cat gtc ttg caa gct gtt cat cca tct    818
Thr Ile Asp Arg Lys Arg His His Val Leu Gln Ala Val His Pro Ser
                255                 260                 265

cct ttg tct gct cat cgt ggg ttc ctt ggt tgt aag cac ttc tcc aag    866
Pro Leu Ser Ala His Arg Gly Phe Leu Gly Cys Lys His Phe Ser Lys
            270                 275                 280

gct aac ggg ctg ctg aaa cta tct ggg acg gag cct ata aac tgg aga    914
Ala Asn Gly Leu Leu Lys Leu Ser Gly Thr Glu Pro Ile Asn Trp Arg
    285                 290                 295

gca ctc taactcttta tgctgcctta tactgttaac tgttttaaga tgaacatcac    970
Ala Leu
300

actatatttt ctacagcttt tccaagttca aaccaatcta taagctttca tttgtctttt 1030

ggaatgatgc tgcttttggt cggttttaga tacttaaaac actttaccac tctgccatgt 1090

tgactcatgt tcagtcaata taactttcac aacttgaaca aaaatgttat tttataattg 1150

attatattct gtacattaaa gattgttttt ttcccaggct gtttcatagg tactaggata 1210

ttaaactgtt attaacctat tttccatgat gtcaactgct taagttttta tgcagaaata 1270

aattatatat tta                                                    1283


<210> 2
<211> 301
<212> PRT
<213> Gadus morhua

<400> 2
Met Leu Phe Lys Leu Gly Leu Cys Gln Arg Cys Ile Ser Ser Asn Arg
  1               5                  10                  15

Val Leu Pro Gly Leu Leu Ile Pro Gln Thr Leu Cys Phe Ser Lys Leu
            20                  25                  30

Met Lys Ile Thr Pro Lys Lys Leu Arg Ser Ser Asn Val Glu Gln Lys
        35                  40                  45
```

3

Thr Ser Ser Pro Gln Leu Ser Val Glu Gln Leu Glu Arg Met Ala Lys
    50   55   60

Asn Lys Lys Ala Ala Leu Asp Lys Ile Arg Ala Lys Ala Thr Pro Ala
65   70   75   80

Gly Phe Gly Glu Thr Trp Arg Arg Glu Leu Ala Ala Glu Phe Glu Lys
                85   90   95

Pro Tyr Phe Lys Gln Leu Met Ser Phe Val Ala Asp Glu Arg Ser Arg
            100   105   110

His Thr Val Tyr Pro Pro Ala Asp Gln Val Tyr Ser Ser Thr Glu Met
        115   120   125

Cys Asp Ile Gln Asp Val Lys Val Val Ile Leu Gly Gln Asp Pro Tyr
    130   135   140

His Gly Pro Asn Gln Ala His Gly Leu Cys Phe Ser Val Gln Lys Pro
145   150   155   160

Val Pro Pro Pro Ser Leu Val Asn Ile Tyr Lys Glu Leu Cys Thr
                165   170   175

Asp Ile Asp Gly Phe Lys His Pro Gly His Gly Asp Leu Ser Gly Trp
            180   185   190

Ala Lys Gln Gly Val Leu Leu Leu Asn Ala Val Leu Thr Val Arg Ala
            195   200   205

His Gln Ala Asn Ser His Lys Asp Arg Gly Trp Glu Thr Phe Thr Asp
    210   215   220

Ala Val Ile Lys Trp Leu Ser Val Asn Arg Glu Gly Val Val Phe Leu
225   230   235   240

Leu Trp Gly Ser Tyr Ala His Lys Lys Gly Ala Thr Ile Asp Arg Lys
                245   250   255

Arg His His Val Leu Gln Ala Val His Pro Ser Pro Leu Ser Ala His
            260   265   270

Arg Gly Phe Leu Gly Cys Lys His Phe Ser Lys Ala Asn Gly Leu Leu
            275   280   285

Lys Leu Ser Gly Thr Glu Pro Ile Asn Trp Arg Ala Leu
    290   295   300

4

<210> 3
<211> 1355
<212> DNA
<213> Gadus morhua

<220>
<221> CDS
<222> (90)..(992)

<400> 3
gatggtttag gaggatagta ctttgacact ggttagcgaa ggggaaaacg gagttattgt 60

gcatatcgtt ttagccctac gtttaaaaa atg att ggt caa cag cat atc aac   113
                                  Met Ile Gly Gln Gln His Ile Asn
                                  1   5

tct ttc ttc tca cca gtt tca aaa aag aga gtt tca aag gaa tta ggt   161
Ser Phe Phe Ser Pro Val Ser Lys Lys Arg Val Ser Lys Glu Leu Gly
      10   15   20

aaa acc gaa aag cat gcc gaa gaa gtt cag ata acg ccg aag aaa ctg   209
Lys Thr Glu Lys His Ala Glu Glu Val Gln Ile Thr Pro Lys Lys Leu
 25   30   35   40

agg tcc tca aat gtg gaa caa aag acg tca tcg cca cag ctt tca gtg   257
Arg Ser Ser Asn Val Glu Gln Lys Thr Ser Ser Pro Gln Leu Ser Val
                 45   50   55

gag cag ctg gaa aga atg gcc aaa aat aag aaa gca gcg ctt gac aag   305
Glu Gln Leu Glu Arg Met Ala Lys Asn Lys Lys Ala Ala Leu Asp Lys
             60   65   70

att aga gca aaa gca acg cct gca ggt ttc gga gag act tgg aga aga   353
Ile Arg Ala Lys Ala Thr Pro Ala Gly Phe Gly Glu Thr Trp Arg Arg
         75   80   85

gag ctg gct gca gag ttt gaa aag cca tac ttc aaa caa ttg atg tcc   401
Glu Leu Ala Ala Glu Phe Glu Lys Pro Tyr Phe Lys Gln Leu Met Ser
     90   95   100

ttt gta gct gat gag agg agc cgt cac acc gtc tac cca ccg gct gat   449
Phe Val Ala Asp Glu Arg Ser Arg His Thr Val Tyr Pro Pro Ala Asp
105   110   115   120

caa gtg tac agt tgg aca gag atg tgt gac att caa gat gtg aaa gta   497
Gln Val Tyr Ser Trp Thr Glu Met Cys Asp Ile Gln Asp Val Lys Val

5

```
gtg att cta ggc cag gac cct tac cac ggt ccc aac caa gca cat gga    545
Val Ile Leu Gly Gln Asp Pro Tyr His Gly Pro Asn Gln Ala His Gly
            140                 145                 150

ctc tgt ttc agt gtg caa aag cca gtt ccc cct ccc ccc agt ctc gtg    593
Leu Cys Phe Ser Val Gln Lys Pro Val Pro Pro Pro Pro Ser Leu Val
            155                 160                 165

aac ata tac aaa gaa ttg tgt acc gac att gat ggc ttc aag cat cct    641
Asn Ile Tyr Lys Glu Leu Cys Thr Asp Ile Asp Gly Phe Lys His Pro
            170                 175                 180

gga cat gga gat cta agc gga tgg gca aac aag ggg tgc tgc tgc tta    689
Gly His Gly Asp Leu Ser Gly Trp Ala Asn Lys Gly Cys Cys Cys Leu
185                     190                 195                 200

acg cgc tgc ctg acc gtg cgg gcc cat cag gcc aac tcc cac aag gac    737
Thr Arg Cys Leu Thr Val Arg Ala His Gln Ala Asn Ser His Lys Asp
                205                 210                 215

aga ggc tgg gag acc tcc acc gac gct gtg atc aag tgg ctg agc gtc    785
Arg Gly Trp Glu Thr Ser Thr Asp Ala Val Ile Lys Trp Leu Ser Val
            220                 225                 230

aac cgg gaa gga gtg gtt ttc ctg ttc tgg ggc tca tac gcc cat aag    833
Asn Arg Glu Gly Val Val Phe Leu Phe Trp Gly Ser Tyr Ala His Lys
            235                 240                 245

aag gga gcg acc atc gac agg aaa cgt cac cat gtc ttg caa gct ctt    881
Lys Gly Ala Thr Ile Asp Arg Lys Arg His His Val Leu Gln Ala Leu
        250                 255                 260

cat cca tct cct ttg tct gct cat cgt ggg ttc ctt ggt tgt aag cac    929
His Pro Ser Pro Leu Ser Ala His Arg Gly Phe Leu Gly Cys Lys His
265                 270                 275                 280

ttc tcc aag gct aac ggg ctg ctg aaa cta tct ggg acg gag cct ata    977
Phe Ser Lys Ala Asn Gly Leu Leu Lys Leu Ser Gly Thr Glu Pro Ile
                285                 290                 295

aac tgg aga gca ctc taactcttta tgctgcctta tactgttaac tgttttaaga   1032
Asn Trp Arg Ala Leu
        300

tgaacatcac actatatttt ctacagcttt tccaagttca aaccaatcta taagctttca   1092
```

tttgtctttt ggaatgatgc tgcttttggt cggttttaga tacttaaaac actttaccac 1152

tctgccatgt tgactcatgt tcagtcaata taactttcac aacttgaaca aaaatgttat 1212

tttataattg attatattct gtacattaaa gattgttttt ttcccaggct gtttcatagg 1272

tactaggata ttaaactgtt attaacctat tttccatgat gtcaactgct taagtttttа 1332

tgcagaaata aattatatat tta 1355

<210> 4
<211> 301
<212> PRT
<213> Gadus morhua

<400> 4
Met Ile Gly Gln Gln His Ile Asn Ser Phe Phe Ser Pro Val Ser Lys
 1   5   10   15

Lys Arg Val Ser Lys Glu Leu Gly Lys Thr Glu Lys His Ala Glu Glu
            20   25   30

Val Gln Ile Thr Pro Lys Lys Leu Arg Ser Ser Asn Val Glu Gln Lys
        35   40   45

Thr Ser Ser Pro Gln Leu Ser Val Glu Gln Leu Glu Arg Met Ala Lys
    50   55   60

Asn Lys Lys Ala Ala Leu Asp Lys Ile Arg Ala Lys Ala Thr Pro Ala
65   70   75   80

Gly Phe Gly Glu Thr Trp Arg Arg Glu Leu Ala Ala Glu Phe Glu Lys
                85   90   95

Pro Tyr Phe Lys Gln Leu Met Ser Phe Val Ala Asp Glu Arg Ser Arg
                100   105   110

His Thr Val Tyr Pro Pro Ala Asp Gln Val Tyr Ser Trp Thr Glu Met
            115   120   125

Cys Asp Ile Gln Asp Val Lys Val Val Ile Leu Gly Gln Asp Pro Tyr
    130   135   140

His Gly Pro Asn Gln Ala His Gly Leu Cys Phe Ser Val Gln Lys Pro
145   150   155   160

Val Pro Pro Pro Pro Ser Leu Val Asn Ile Tyr Lys Glu Leu Cys Thr

7

```
              165                    170                    175

Asp Ile Asp Gly Phe Lys His Pro Gly His Gly Asp Leu Ser Gly Trp
            180                185                190

Ala Asn Lys Gly Cys Cys Cys Leu Thr Arg Cys Leu Thr Val Arg Ala
            195                200                205

His Gln Ala Asn Ser His Lys Asp Arg Gly Trp Glu Thr Ser Thr Asp
    210                215                220

Ala Val Ile Lys Trp Leu Ser Val Asn Arg Glu Gly Val Val Phe Leu
225                230                235                240

Phe Trp Gly Ser Tyr Ala His Lys Lys Gly Ala Thr Ile Asp Arg Lys
            245                250                255

Arg His His Val Leu Gln Ala Leu His Pro Ser Pro Leu Ser Ala His
            260                265                270

Arg Gly Phe Leu Gly Cys Lys His Phe Ser Lys Ala Asn Gly Leu Leu
            275                280                285

Lys Leu Ser Gly Thr Glu Pro Ile Asn Trp Arg Ala Leu
    290                295                300


<210> 5
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
      Sequence - Primer used to generate cDNA of a
      fragment of UNG gene

<400> 5
tacggctgcg agaagacgac agaaggg                                    27


<210> 6
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
```

Sequence - Primer used to prepare cDNA of a
fragment of UNG gene

<400> 6
tacggctccg agaagacgac agaa   24

<210> 7
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
      Sequence - Primer used to generate cDNA portion
      of cUNG gene

<400> 7
gghcargayc cctayca   17

<210> 8
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
      Sequence - Primer used to generate cDNA portion of
      gene

<400> 8
dccccasags agraavac   18

<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
      Sequence - Primer used to generate fragment of UNG
      gene

<400> 9
tgtaccgaca ttgatggctt caagcat   27

```
<210> 10
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
      Sequence - Primer used to generate fragment of UNG
      gene

<400> 10
cccatccgct tagatctcca tgtccag                                      27


<210> 11
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
      Sequence - Primer used to generate fragment of UNG
      gene

<400> 11
ccatcctaat acgactcact atagggc                                      27


<210> 12
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
      Sequence - Primer used to generate fragment of
      RACE fragment of UNG gene

<400> 12
atggaattcg attgagattg gcgcctttgg                                   30


<210> 13
<211> 30
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Artificial
       Sequence - Primer used to construct rcUNG delta 74
       gene

<400> 13
accatggaat tcccaaaagc aacgcctgca   30

<210> 14
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
       Sequence - Primer used to construct rcUNG delta 74
       gene

<400> 14
gagctcgtcg acttagagtg cctctccagt ttatagg   37

<210> 15
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
       Sequence - Primer used to construct rcUNG delta 81
       gene

<400> 15
accatggaat tcttcggaga gacttggaga aga   33

<210> 16
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
       Sequence - Primer used to construct rcUNG delta
       74o   gene

<400> 16

11

atggaattcg caaaagcaac gcctgcaggt ttcggagaga cttggcgtcg tcag   54

<210> 17
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
      Sequence - Primer used to construct rcUNG delta
      81o gene

<400> 17
atggaattct tcggagagac ttggcgtcgt tgagctggct gc   42

<210> 18
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
      Sequence - Primer used to prepare rcUNG gene

<400> 18
tctctcgaga aaagagaggc tgaagctccc attgacgatg aggatga   47

<210> 19
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial
      Sequence - Primer used to prepare rcUNG gene

<400> 19
gtagaattcg gatccatgtc tcctccagtc tagat   35